```
            Query Match            52.0%;  Score 3614;  DB 1;  Length 1201;
            Best Local Similarity  55.5%;  Pred. No. 1.1e-180;
            Matches  665;  Conservative  145;  Mismatches  236;  Indels  152;  Gaps  17;

Qy     37  DYGVTVPCSTDFRGRFLSHVVSGPAAASAGSMVVDTPPTLPRHSSHLR-----VARSPLH  91
           :|  :  |  ||: ||:|||  :|                            :||  :    |: :|
Db     37  EYELVTPVSTNLEGRYLSHTLS--------------------ASHKKRSARDVSSNP--  73

Qy     92  PGGTLWPGRVGRHSLYFNVTVFGKELHLRLRPNRRLVVPGSSVEWQE-------------  138
                        |:||:|  |||: ||||:|| :||  ||: |||  |
Db     74  -----------EQLFFNITAFGKDFHLRLKPNTQLVAPGAVVEWHETSLVPGNITDPIN  121

Qy    139  -------DFRELFRQPLRQECVYTGGVTGMPGAAVAISNCDGLAGLIRTDSTDFFIEPLE  191
                  :|      :||:   | | |  :   :||  :||||||||||||:|::|:  ::||||||
Db    122  NHQPGSATYRIRKTEPLQTNCAYVGDIVDIPGTSVAISNCDGLAGMIKSDNEEYFIEPLE  181

Qy    192  RGQQEKEASGRTHVVYRREAVQQEWAEPDGDLH---NEAFGLGDLPNLLGLVGDQLGDTE  248
           ||:|  :|   ||  ||||:| ||:|      :      | |   ::  || ||  : |    || :|
Db    182  RGKQMEEEKGRIHVVYKRSAVEQAPIDMSKDFHYRESDLEGLDDLGTVYGNIHQQLNETM  241

      249  RKRRHAKPGSYSIEVLLVVDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESLGVHINIAL  308
           |:||||    |:|||||   ||||||||||||||||||||:||||||:||||||||||||||: |
      242  RRRRHAGENDYNIEVLLGVDDSVVRFHGKEHVQNYLLTLMNIVNEIYHDESLGVHINVVL  301

Qy    309  VRLIMVGYRQSLSLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHHDHVVFLTRQDFGPS-  367
           ||:||:|:||  :|:|||||||||||||||||||  ||||    ||| :|:||||  :||||||||||
Db    302  VRMIMLGYAKSISLIERGNPSRSLENVCRWASQQQRSDLNHSEHHDHAIFLTRQDFGPAG  361

Qy    368  --GYAPVTGMCHPLRSCALNHEDGFSSAFVIAHETGHVLGMEHDGQGNGCADETSLGSVM  425
             ||||||||||||:|||  |||||||||||||||:||||||||||||||||||||  | |||::|||
Db    362  MQGYAPVTGMCHPVRSCTLNHEDGFSSAFVVAHETGHVLGMEHDGQGNRCGDETAMGSVM  421

Qy    426  APLVQAAFHRFHWSRCSKLELSRYLPSYDCLLDDPFDPAWPQPPELPGINYSMDEQCRFD  485
           |||||||||||:||||||  || ||:  ||||||||||||:  ||:  |||||||||||||||
Db    422  APLVQAAFHRYHWSRCSGQELKRYIHSYDCLLDDPFDHDWPKLPELPGINYSMDEQCRFD  481

Qy    486  FGSGYQTCLAFRTFEPCKQLWCSHPDNPYFCKTKKGPPLDGTECAPGKWCFKGHCIWKSP  545
           || ||:  |  |||||:| ||||||||||||||||||||||||||||||  |||||||::|:|::
Db    482  FGVGYKMCTAFRTFDPCKQLWCSHPDNPYFCKTKKGPPLDGTECAAGKWCYKGHCMWKNA  541

Qy    546  EQTYGQDGGWSSWTKFGSCSRSCGGGVRSRSRSCNNPSPAYGGRPCLGPMFEYQVCNSEE  605
            |    ||| |||||||||||:||  |||  |:|  ||||  |  ||:  | |    ||||:||:|||
Db    542  NQ-QKQDGNWGSWTKFGSCSRTCGTGVRFRTRQCNNPMPINGGQDCPGVNFEYQLCNTEE  600

Qy    606  CPGTYEDFRAQQCAKRNSYYVHQNAKHSWVPYEPDDDAQKCELICQSADTGDVVFMNQVV  665
           |    :||||||||| :|||::  :||  ||  |:|||     :|  | |||  :|||||  :| .|:|
Db    601  CQKHFEDFRAQQCQQRNSHFEYQNTKHHWLPYEHPDPKKRCHLYCQSKETGDVAYMKQLV  660

Qy    666  HDGTRCSYRDPYSVCARGECVPVGCDKEVGSMKADDKCGVCGGDNSHCRTVKGTLGKASK  725
           ||||  |||:||||:|| |||||  ||||||  ||:|  | :||||||||||||||||||  :  :
Db    661  HDGTHCSYKDPYSICVRGECVKVGCDKEIGSNKVEDKCGVCGGDNSHCRTVKGTFTRTPR  720

Qy    726  QAGALKLVQIPAGARHIQIEALEKSPHRSVVKNQVTGSFILNPKGKEATSRTFTAMGLEW  785
           :  |  ||:   ||  ||||: |:    |   |||    :||| |:||| ||::|  ||||    :|:||
Db    721  KLGYLKMFDIPPGARHVLIQEDEASPHILAIKNQATGHYILNGKGEEAKSRTFIDLGVEW  780

Qy    786  EDAVEDAKESLKTSGPLPEAIAILALPPTEGGPRSSLAYKYVIHEDLLPLIGSNNVLLEE  845
           :  :||   ||| |  | |  |||  :  : :|  ||    ||||  ||||||  :|  ||||  ||
Db    781  DYNIEDDIESLHTDGPLHDPVIVLII-PQENDTRSSLTYKYIIHEDSVPTINSNNVIQEE  839

Qy    846  MDTYEWALKSWAPCSKACGGGIQFTKYGCRRRRDHHMVQRHLCDHKKRPKPIRRRCNQHP  905
           :||:||||||||:   ||  ||||  |:|||||||||:  |: ||  | |:||||||||||||
Db    840  LDTFEWALKSWSQVSKPCGGGFQYTKYGCRRKSDNKMVHRSFCEANKKPKPIRRMCNIQE  899

Qy    906  CSQPVWVTEEWGACSRSCGKLGVQTRGIQCLLPLSNGTHKVMPAKACAGDRPEARRPCLR  965
           |: |:|| |||  |:::||   |||  | | ::|| ||  ||::  : :|  |||||:||||| |
Db    900  CTHPLWVAEEWEHCTKTCGSSGYQLRTVRCLQPLLDGTNRSVHSKYCMGDRPESRRPCNR  959

Qy    966  VPCPAQWRLGAWSQCSATCGEGIQQRQVVCRTNANSLGHCEGDRPDTVQVCSLPACGGNH  1025
           ||||||: | ||:|| ||||| : |||:||         ||:|:|::|:|: | ||| |
Db    960  VPCPAQWKTGPWSECSVTCGEGTEVRQVLCRAG----DHCDGEKPESVRACQLPPCND--  1013

Qy   1026  QNSTVRADVWELGTPEGQWVPQSGPLHPINKISSMCAAEPCTGDRSVFCQMEVLDRYCSI  1085
                                                   ||| ||:|:||||||| |||||
Db   1014  ------------------------------------EPCLGDKSIFCQMEVLARYCSI  1035

Qy   1086  PGYHRLCCVSCIKKASG----------------PNPGPDPG----PTSLPPF--STPG-  1121
           |||::|||| || |:::                             ||  |    |||| |:    ||
Db   1036  PGYNKLCCESCSKRSSTLPPPYLLEAAETHDDVISNPSDLPRSLVMPTSLVPYHSETPAK  1095

Qy   1122  -------SPLPGPQDPADAAEPPGKPTGSEDHQHGRATQLPGALDT------SSPGTQ  1166
                  |: ||   |  |   |  ||  |   |  |: |  |:            |||  |:
Db   1096  KMSLSSISSVGGPNAYA-AFRPNSKPDGANLRQ--RSAQQAGSKTVRLVTVPSSPPTK  1150
```

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ID   ATS3_HUMAN      STANDARD;      PRT;   1201 AA.
AC   O15072;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ADAMTS-3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE   with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS3) (Fragment).
GN   ADAMTS3 OR KIAA0366.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97349984; PubMed=9205841;
RA   Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
RA   Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. VII.
RT   The complete sequences of 100 new cDNA clones from brain which can
RT   code for large proteins in vitro.";
RL   DNA Res. 4:141-150(1997).
CC   -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: SECRETED. ASSOCIATED WITH THE EXTRACELLULAR
CC       MATRIX (BY SIMILARITY).
CC   -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT
CC       FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX.
CC   -!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
CC   -!- SIMILARITY: CONTAINS 1 DISINTEGRIN-LIKE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS.
CC   -!- CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB002364; BAA20821.1; -.
DR   MEROPS; M12.220; -.
DR   MIM; 605011; -.
DR   InterPro; IPR001762; Disintegrin.
DR   InterPro; IPR002870; Pep_M12B_propep.
DR   InterPro; IPR001590; Reprolysin.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01562; Pep_M12B_propep; 1.
DR   Pfam; PF01421; Reprolysin; 1.
DR   Pfam; PF00090; tsp_1; 4.
DR   SMART; SM00209; TSP1; 4.
DR   PROSITE; PS50215; ADAM_MEPRO; 1.
DR   PROSITE; PS50092; TSP1; 2.
DR   PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
DR   PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
KW   Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
KW   Repeat; Extracellular matrix; Heparin-binding.
FT   NON_TER        1      1
FT   SIGNAL        <1      ?       POTENTIAL.
FT   PROPEP         ?    245       BY SIMILARITY.
FT   CHAIN        246   1201       ADAMTS-3.
FT   METAL        394    394       ZINC (CATALYTIC) (BY SIMILARITY).
FT   ACT_SITE     395    395       BY SIMILARITY.
FT   METAL        398    398       ZINC (CATALYTIC) (BY SIMILARITY).
FT   METAL        404    404       ZINC (CATALYTIC) (BY SIMILARITY).
FT   DOMAIN       466    546       DISINTEGRIN-LIKE.
FT   DOMAIN       547    603       TSP TYPE-1 1.
FT   DOMAIN       604    708       CYS-RICH.
FT   DOMAIN       709    840       SPACER.
FT   DOMAIN       841    898       TSP TYPE-1 2.
     DOMAIN       899    961       TSP TYPE-1 3.
     DOMAIN       962   1013       TSP TYPE-1 4.
     DOMAIN       242    245       POLY-ARG.
     CARBOHYD      79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     471    471       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     810    810       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     938    938       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1201 AA;  135113 MW;  D54EA92BD506A3AA CRC64;
```